



PTO/SB/08a/b (08-03)

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<b>Substitute for form 1449A/B/PTO</b>  <b>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</b>  (Use as many sheets as necessary)			<b>Complete If Known</b>		
			Application Number	09/745920	
			Filing Date	December 21, 2000	
			First Named Inventor	PARKER, Kenneth C.	
			Art Unit	1631	
			Examiner Name	Smith, Carolyn L.	
Sheet	1	of	3	Attorney Docket Number	SY9-155

U.S. PATENT DOCUMENTS					
Examiner Initials*	Cite No. <sup>1</sup>	Document Number	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
		Number-Kind Code <sup>2</sup> (if known)			
AS	A2	5,538,897	07-23-1996	Yates III et al.	

FOREIGN PATENT DOCUMENTS						
Examiner Initials*	Cite No. <sup>1</sup>	Foreign Patent Document	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T <sup>3</sup>
		Country Code <sup>3</sup> -Number <sup>4</sup> -Kind Code <sup>5</sup> (if known)				

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NON PATENT LITERATURE DOCUMENTS							
Examiner Initials*	Cite No. <sup>1</sup>	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.				T <sup>2</sup>	
AS	C5	Anderegg et al. "Correction of the cDNA-derived protein sequence of prostatic spermine binding protein: pivotal role of tandem mass spectrometry in sequence analysis." <i>Biochemistry</i> . 1988 Jun 14;27(12):4214-21.					
	C6	Bartels et al. "Fast algorithm for peptide sequencing by mass spectroscopy." <i>Biomedical and Environmental Mass Spectrometry</i> 19:363-368 (1990).					
	C7	Biemann et al. "Characterization by tandem mass spectrometry of structural modifications in proteins." <i>Science</i> . 1987 Aug 28;237(4818):992-8.					
	C8	Biemann "Mass spectrometry of peptides and proteins." <i>Annu Rev Biochem</i> . 1992;61:977-1010.					
	C9	Biemann "Sequencing of peptides by tandem mass spectrometry and high-energy collision-induced dissociation." <i>Methods Enzymol</i> . 1990;193:455-79.					
	C10	Falick et al. "Low-mass ions produced from peptides by high-energy collision-induced dissociation in tandem mass spectrometry." <i>J. Am. Soc. Mass Spectrom</i> . 4:882-893 (1993).					
	C11	Griffin et al. "The amino acid sequence of the sex steroid-binding protein of rabbit serum." <i>J Biol Chem</i> . 1989 Nov 15;264(32):19066-75.					
	C12	Hamm et al. "Peptide sequencing program." <i>Comput Appl Biosci</i> . 1986 Jun;2(2):115-8.					
	C13	Henderson et al. "HLA-A2.1-associated peptides from a mutant cell line: a second pathway of antigen presentation." <i>Science</i> . 1992 Mar 6;255(5049):1264-6.					
	C14	Hines et al. "Pattern-based algorithm for peptide sequencing from tandem high energy collision-induced dissociation mass spectra." <i>J. Am. Soc. Mass Spectrom</i> . 3:326-336 (1992).					
	C15	Hunt et al. "Protein sequencing by tandem mass spectrometry." <i>Proc Natl Acad Sci U S A</i> . 1986 Sep;83(17):6233-7.					
	Examiner Signature		Date Considered			10/27/2005	



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			Examiner Name	Smith, Carolyn L.	
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AS	C16	Ishikawa <i>et al.</i> "Computer-aided peptide sequencing by fast atom bombardment mass spectrometry." <i>Biomedical and Environmental Mass Spectrometry</i> . 13:373-80 (1986).		
	C17	Ishikawa <i>et al.</i> "Sequence determination of unknown cyclic peptide antibiotics by fast atom bombardment mass spectrometry." <i>Biomedical and Environmental Mass Spectrometry</i> 19:395-399 (1990).		
	C18	James <i>et al.</i> "Protein identification by mass profile fingerprinting." <i>Biochemical and biophysical research communications</i> 195(1):58-64 (1993).		
	C19	Johnson <i>et al.</i> "Computer program (SEQPEP) to aid in the interpretation of high-energy collision tandem mass spectra of peptides." <i>Biomed Environ Mass Spectrom</i> . 1989 Nov;18(11):945-57.		
	C20	Johnson <i>et al.</i> "The primary structure of thioredoxin from <i>Chromatium vinosum</i> determined by high-performance tandem mass spectrometry." <i>Biochemistry</i> . 1987 Mar 10;26(5):1209-14.		
	C21	Johnson <i>et al.</i> "Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined by tandem mass spectrometry." <i>J Biol Chem</i> . 1988 Jul 15;263(20):9589-97.		
	C22	Johnson "Determination of peptide and protein structure by tandem mass spectrometry." pp.1-361 Diss. Massachusetts Institute of Technology, Cambridge (1988).		
	C23	Johnson <i>et al.</i> "Sequence analysis of peptide mixtures by automated integration of Edman and mass spectrometric data." <i>Protein Science</i> 1:1083-91 (1992).		
	C24	Kaur <i>et al.</i> "Characterization of structural xenobiotic modifications in proteins by high sensitivity tandem mass spectrometry. Human hemoglobin treated in vitro with styrene 7,8-oxide." <i>J Biol Chem</i> . 1989 Oct 15;264(29):16981-4.		
	C25	Kokame <i>et al.</i> "Lipid modification at the N terminus of photoreceptor G-protein alpha-subunit." <i>Nature</i> . 1992 Oct 22;359(6397):749-52.		
	C26	Leef <i>et al.</i> "MacProMass: a computer program to correlate mass spectral data to peptide and protein structures." <i>Biomedical and Environmental Mass Spectrometry</i> 19:639-45 (1990).		
	C27	Mann <i>et al.</i> "Error-tolerant identification of peptides in sequence databases by peptide sequence tags." <i>Anal Chem</i> . 1994 Dec 15;66(24):4390-9.		
	C28	Neubert <i>et al.</i> "The rod transducin alpha subunit amino terminus is heterogeneously fatty acylated." <i>J Biol Chem</i> . 1992 Sep 15;267(26):18274-7.		
	C29	Sakurai <i>et al.</i> "PAAS 3: a computer program to determine probable sequence of peptides from mass spectrometric data." <i>Biomedical Mass Spectrometry</i> 1984; 11(8):395-399.		
	C30	Scoble <i>et al.</i> "A graphics display-oriented strategy for the amino acid sequencing of peptides by tandem mass spectrometry." <i>Fresenius Z. Anal. Chem</i> . 1987; 327:239-45.		
	C31	Siegel <i>et al.</i> "An efficient algorithm for sequencing peptides using fast atom bombardment mass spectral data." <i>Biomedical and Environmental Mass Spectrometry</i> 1988; 15:333-343.		
	C32	Watkins <i>et al.</i> "Mass spectrometry software for biochemical analysis in electrospray and fast atom bombardment modes." <i>BCSTBS</i> 1991; 19(4) 7 pp..		
	C33	Yates III <i>et al.</i> "Peptide mass maps: a highly informative approach to protein identification." <i>Analytical Biochemistry</i> 1993; 214:397-408.		

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CS	C34	Yates III <i>et al.</i> "Computer aided interpretation of low energy MS/MS mass spectra of peptides." 1991; Chapter 46, pp. 477-485 in <u>Techniques in Protein Chemistry II</u> , Villafranca ed., Academic Press, Inc., Boston.	

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